(FILE 'HOME' ENTERED AT 14:56:05 ON 23 DEC 2002)

FILE 'BIOSIS, MEDLINE, CAPLUS, EMBASE, SCISEARCH' ENTERED AT 14:56:39 ON 23 DEC 2002

L1	7469	S	ATP BINDING SITE
L2	2054320	S	MUTANT OR MUTATION OR SUBSTITUTION
L3	48076	S	MITOGEN ACTIVATION PROTEIN KINASE OR MAP KINASE
L4	60	S	L1 AND L2 AND L3
L5	26		DUPLICATE REMOVE L4 (34 DUPLICATES REMOVED)
L6	11219	S	EXTRACELLULAR-SIGNAL REGULATED KINASE 2 OR ERK2
L7	14	S	L1 AND L2 AND L6
L8	5		DUPLICATE REMOVE L7 (9 DUPLICATES REMOVED)
L9	404	S	JUN-N-TERMINAL KINASE 3 OR JNK3
L10	1	S	L1 AND L2 AND L9
L11	179886	S	SERINE-THREONINE KINASE OR TYROSINE KINASE
L12	428	S	L1 AND L2 AND L11
L13	27955	S	SERINE-THREONINE KINASE
L14	76	S	L1 AND L2 AND L13
L15	36		DUPLICATE REMOVE L14 (40 DUPLICATES REMOVED)
L16	156802	S	TYROSINE KINASE
L17	372	S	L1 AND L2 AND L16
L18	2985652	S	BINDING
L19	372	S	L17 AND L18
L20	26367	S	BINDING CONSTANT
L21	0	S	L17 AND L20

L15 ANSWER 21 OF 36 MEDLINE
AN 97306066 MEDLINE
DN 97306066 PubMed ID: 9163534
TI Studies on the site of phosphorylation of Ca2+/calmodulin-dependent protein kinase (CaM-kinase) IV by CaM-kinase kinase.
AU Kitani T; Okuno S; Fujisawa H
CS Department of Biochemistry, Asahikawa Medical College, Hokkaido.
SO JOURNAL OF BIOCHEMISTRY, (1997 Apr) 121 (4) 804-10.
Journal code: 0376600. ISSN: 0021-924X.
CY Japan
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199707
ED Entered STN: 19970812
Last Updated on STN: 20020420
Entered Medline: 19970729
AB The phosphorylation site(s) involved in the activation of CaM-kinase IV by CaM-kinase kinase alpha was studied using a **mutant** CaM-kinase IV (K71R) in which Lys71 (**ATP-binding site**) was replaced with Arg, because the autophosphorylation of CaM-kinase IV occurring at multiple sites made it difficult to study phosphorylation of the enzyme by CaM-kinase kinase. Sequence analysis of the phosphopeptide from the trypsin digest of CaM-kinase IV (K71R) phosphorylated by CaM-kinase kinase alpha suggested that the phosphorylation of CaM-kinase IV by CaM-kinase kinase only occurred at Thr196. The recombinant **mutant** CaM-kinase IV in which Thr196 or Thr200 was replaced with nonphosphorylatable alanine showed little activity in the presence and absence of the kinase kinase. The **mutant** enzyme in which Thr196 was replaced with negatively charged aspartic acid showed almost 25 times as high activity as the wild-type enzyme in the absence of the kinase kinase, and no more activation was observed in its presence. In contrast, the enzyme in which Thr200 was replaced with aspartic acid showed little enzyme activity. Thus, it may be concluded that the phosphorylation of Thr196 in CaM-kinase IV by CaM-kinase kinase is necessary for the subsequent autophosphorylation and activation of CaM-kinase IV.
CT Check Tags: Support, Non-U.S. Gov't
Amino Acid Sequence
Arginine: ME, metabolism

L5 ANSWER 24 OF 26 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC. DUPLICATE 9

AN 1994:14476 BIOSIS

DN PREV199497027476

TI Activity of the yeast **MAP kinase** homologue Slt2 is critically required for cell integrity at 37 degree C.

AU Martin, Humberto; Arroyo, Javier; Sanchez, Miguel; Molina, Maria; Nombela, Cesar (1)

CS (1) Dep. Microbiol. II, Fac. Farmacia, Universidad Complutense, E28040 Madrid Spain

SO Molecular & General Genetics, (1993) Vol. 241, No. 1-2, pp. 177-184. ISSN: 0026-8925.

DT Article

LA English

AB Deletion of the SLT2 gene of Saccharomyces cerevisiae, which codes for a homologue of MAP (mitogen-activated) protein kinases, causes an autolytic lethal phenotype in cells grown at 37 degree C. The gene encodes domains characteristic of protein kinases, which include a lysine (at position 54) that lies 19 residues from a glycine-rich cluster, considered to be the putative **ATP binding site**. The ability of three **mutant** alleles of SLT2 generated by site-directed mutagenesis, namely E54 (glutamic acid), R54 (arginine) and F54 (phenylalanine), to complement slt2 **mutants** was tested. All three failed to complement the autolytic phenotype and were unable to restore growth and viability of cells. A strain obtained by transplacement of slt2-F54 also behaved as a thermosensitive autolytic **mutant**. By immunoprecipitation with polyclonal antibodies raised against Slt2 protein expressed in Escherichia coli, it was possible to confirm that alteration of the lysine-54 residue did not affect the stability of the protein, thus allowing us to conclude that activity of the Slt2 protein kinase is critically required for growth and morphogenesis of S. cerevisiae at 37 degree C. A significant fraction of the **mutant** cell population lysed at 24 degree C and the cells displayed a characteristic alteration of the surface consisting of a typical depression in an area of the cell wall. At 37 degree C, the cell surface was clearly disorganized.

L5 ANSWER 20 OF 26 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 8

AN 1994:298744 BIOSIS

DN PREV199497311744

TI The level of insulin receptor tyrosine kinase activity modulates the activities of phosphatidylinositol 3-kinase, microtubule-associated protein, and S6 kinases.

AU Wilden, Peter A.; Kahn, C. Ronald (1)

CS (1) Res. Div., Room 620, Joslin Diabetes Center, One Joslin Place, Boston, MA 02215 USA

SO Molecular Endocrinology, (1994) Vol. 8, No. 5, pp. 558-567.
ISSN: 0888-8809.

DT Article

LA English

AB The role of insulin receptor tyrosine kinase activity in stimulation of intracellular enzymes linked to insulin action (phosphatidylinositol 3-kinase (Ptdlns 3-kinase), microtubule-associated protein (**MAP**) **kinase**, and S6 kinases) was studied in Chinese hamster ovary cells which overexpress wild type human insulin receptors, receptors with reduced kinase activity due to **substitution** of Phe for Tyr-1146 (single-Phe), Tyr-1150,1151 (double-Phe), and Tyr-1146,1150,1151 (triple-Phe), or kinase-inactive receptors with a **substitution** of Ala for Lys-1018 in the **ATP binding site** (A1018). We have previously shown that receptor autophosphorylation and kinase activity of these **mutants** were reduced by approximately 50, 65, 85, and 100%, respectively. Glycogen and DNA synthesis parallel the level of receptor autophosphorylation and kinase activity; however, receptor serine and threonine phosphorylation was independent of receptor tyrosine kinase activity and receptor internalization was completely dependent on maximal receptor kinase activity. Overexpression of the wild type insulin receptor increased both maximal insulin receptor substrate-1-associated and total insulin-stimulated Ptdlns 3-kinase activity, as well as S6 and **MAP kinase** activities 2.0- to 3.6-fold. In addition there was a leftward shift of the dose-response curves for Ptdlns 3-kinase and S6 kinases by approximately 10-fold. Expression of the single- and double-Phe **mutant** receptors also enhanced maximal Ptdlns 3-kinase activity, but had no effect on insulin sensitivity, whereas expression of either the triple-Phe or kinase-inactive receptors did not enhance insulin stimulation or increase insulin sensitivity as compared to the control cells. When comparing the **mutant** and wild type receptors, differences in insulin sensitivity were least for insulin-stimulated **MAP kinase** and greatest for S6 kinase; with the latter there was greater than a 1000-fold difference in insulin sensitivity when cells that overexpress wild type vs. kinase-inactive insulin receptors were compared. Thus, the level of insulin receptor tyrosine autophosphorylation and kinase activity regulate both maximal activation and insulin sensitivity of these intracellular kinases in the insulin action pathway which may lead to glycogen and/or DNA synthesis. The differential sensitivity of these enzymes to changes in receptor activation suggests that they may be differently coupled to the receptor kinase.

CC Cytology and Cytochemistry - Animal *02506
Genetics and Cytogenetics - Animal *03506
Biochemical Methods - Proteins, Peptides and Amino Acids *10054
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Biochemical Studies - Carbohydrates 10068
Biophysics - General Biophysical Techniques 10504
Biophysics - Molecular Properties and Macromolecules *10506
Biophysics - Membrane Phenomena *10508
Enzymes - Methods 10804

L15 ANSWER 28 OF 36 MEDLINE
AN 94292520 MEDLINE
DN 94292520 PubMed ID: 8021267
TI atpk1, a novel ribosomal protein kinase gene from Arabidopsis. II. Functional and biochemical analysis of the encoded protein.
AU Zhang S H; Broome M A; Lawton M A; Hunter T; Lamb C J
CS Plant Biology Laboratory, Salk Institute for Biological Studies, La Jolla, California 92037.
NC CA 37980 (NCI)
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1994 Jul 1) 269 (26) 17593-9. Journal code: 2985121R. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-L29030
EM 199407
ED Entered STN: 19940815
Last Updated on STN: 20020420
Entered Medline: 19940729
AB The Arabidopsis Atpk1 protein expressed in insect cells and plant cells exhibited multiple sizes consisting mainly of two doublets: p70 (68 and 70 kDa) and p85 (82 and 85 kDa). Extraction of p85 from cells required the presence of SDS, suggesting that p85 is associated with less soluble subcellular components. p70 was extracted by nonionic detergent without SDS, indicating that this form is cytoplasmic. p70 expressed in either Arabidopsis or insect cells underwent serine-specific autophosphorylation, indicating that Atpk1 is a protein-serine kinase. A point **mutation** (lysine 163 to arginine) in the **ATP-binding site** of the catalytic domain substantially diminished activity when expressed in insect cells. A 14-kDa protein (p14) was co-immunoprecipitated with p70 from insect cells expressing wild-type Atpk1 and was phosphorylated in immune complex kinase assays with Atpk1, suggesting it is a homolog of a natural substrate of Atpk1. Two plant ribosomal proteins (14 and 16 kDa) can be phosphorylated by the Atpk1 protein kinase, and we propose that Atpk1 is a novel ribosomal protein kinase. A 60-kDa form of Atpk1 derived from the insect cell-expressed p70 was more highly phosphorylated than p70 in in vitro kinase assays, suggesting a negative regulatory domain can be removed by proteolysis.
CT Check Tags: Animal; Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.
*Arabidopsis: EN, enzymology
Baculoviridae: GE, genetics
Cells, Cultured
Cloning, Molecular
Enzyme Activation
Genes, Plant
Hydrolysis
Moths
Plant Proteins: GE, genetics
*Plant Proteins: ME, metabolism
Protein Processing, Post-Translational
Protein-Serine-Threonine Kinases: GE, genetics
***Protein-Serine-Threonine Kinases: ME, metabolism**
*Ribosomes: EN, enzymology
Substrate Specificity
CN 0 (Plant Proteins); EC 2.7.1.- (Protein-**Serine-Threonine Kinases**); EC 2.7.1.- (atpk1 protein)